```
   1 GGAAGGTTTAAAGAAGAAGCCGCAAAGCGCAGGGAAGGCCTCCCGGCACGGGTGGGGGAAAGCGGCCGGTGCAGCGCGGGGACAGGCACTCGGGCTGGCACTGGCTGCTAGGGATGTCGT
-31                                                                                                                        M  S  S

 121 CCTGGATAAGGTGGCATGGACCCGCCATGGCGCGGCTCTGGGGCTTCTGCTGGCTGGTTGTGGGCTTCTGGAGGGCCGCTTTCGCCTGTCCCACGTCCTGCAAATGCAGTGCCTCTCGGA
-28   W  I  R  W  H  G  P  A  M  A  R  L  W  G  F  C  W  L  V  V  G  F  W  R  A  A  F  A  C  P  T  S  C  K  C  S  A  S  R  I
                                                                                                                +1

 241 TCTGGTGCAGCGACCCTTCTCCTGGCATCGTGGCATTTCCGAGATTGGAGCCTAACAGTGTAGATCCTGAGAACATCACCGAAATTTTCATCGCAAACCAGAAAAGGTTAGAAATCATCA
  13   W  C  S  D  P  S  P  G  I  V  A  F  P  R  L  E  P  N  S  V  D  P  E  N  I  T  E  I  F  I  A  N  Q  K  R  L  E  I  I  N

 361 ACGAAGATGATGTTGAAGCTTATGTGGGACTGAGAAATCTGACAATTGTGGATTCTGGATTAAAATTTGTGGCTCATAAAGCATTTCTGAAAAACAGCAACCTGCAGCACATCAATTTTA
  53   E  D  D  V  E  A  Y  V  G  L  R  N  L  T  I  V  D  S  G  L  K  F  V  A  H  K  A  F  L  K  N  S  N  L  Q  H  I  N  F  T

 481 CCCGAAACAAACTGACGAGTTTGTCTAGGAAACATTTCCGTCACCTTGACTTGTCTGAACTGATCCTGGTGGGCAATCCATTTACATGCTCCTGTGACATTATGTGGATCAAGACTCTCC
  93   R  N  K  L  T  S  L  S  R  K  H  F  R  H  L  D  L  S  E  L  I  L  V  G  N  P  F  T  C  S  C  D  I  M  W  I  K  T  L  Q

 601 AAGAGGCTAAATCCAGTCCAGACACTCAGGATTTGTACTGCCTGAATGAAAGCAGCAAGAATATTCCCCTGGCAAACCTGCAGATACCCAATTGTGGTTTGCCATCTGCAAATCTGGCCG
 133   E  A  K  S  S  P  D  T  Q  D  L  Y  C  L  N  E  S  S  K  N  I  P  L  A  N  L  Q  I  P  N  C  G  L  P  S  A  N  L  A  A

 721 CACCTAACCTCACTGTGGAGGAAGGAAAGTCTATCACATTATCCTGTAGTGTGGCAGGTGATCCGGTTCCTAATATGTATTGGGATGTTGGTAACCTGGTTTCCAAACATATGAATGAAA
 173   P  N  L  T  V  E  E  G  K  S  I  T  L  S  C  S  V  A  G  D  P  V  P  N  M  Y  W  D  V  G  N  L  V  S  K  H  M  N  E  T

 841 CAAGCCACACACAGGGCTCCTTAAGGATAACTAACATTTCATCCGATGACAGTGGGAAGCAGATCTCTTGTGTGGCGGAAAATCTTGTAGGAGAAGATCAAGATTCTGTCAACCTCACTG
 213   S  H  T  Q  G  S  L  R  I  T  N  I  S  S  D  D  S  G  K  Q  I  S  C  V  A  E  N  L  V  G  E  D  Q  D  S  V  N  L  T  V

 961 TGCATTTTGCACCAACTATCACATTTCTCGAATCTCCAACCTCAGACCACCACTGGTGCATTCCATTCACTGTGAAAGGCAACCCAAAACCAGCGCTTCAGTGGTTCTATAACGGGGCAA
 253   H  F  A  P  T  I  T  F  L  E  S  P  T  S  D  H  H  W  C  I  P  F  T  V  K  G  N  P  K  P  A  L  Q  W  F  Y  N  G  A  I

1081 TATTGAATGAGTCCAAATACATCTGTACTAAAATACATGTTACCAATCACACGGAGTACCACGGCTGCCTCCAGCTGGATAATCCCACTCACATGAACAATGGGGACTACACTCTAATAG
 293   L  N  E  S  K  Y  I  C  T  K  I  H  V  T  N  H  T  E  Y  H  G  C  L  Q  L  D  N  P  T  H  M  N  N  G  D  Y  T  L  I  A

1201 CCAAGAATGAGTATGGGAAGGATGAGAAACAGATTTCTGCTCACTTCATGGGCTGGCCTGGAATTGACGATGGTGCAAACCCAAATTATCCTGATGTAATTTATGAAGATTATGGAACTG
 333   K  N  E  Y  G  K  D  E  K  Q  I  S  A  H  F  M  G  W  P  G  I  D  D  G  A  N  P  N  Y  P  D  V  I  Y  E  D  Y  G  T  A

1321 CAGCGAATGACATCGGGGACACCACGAACAGAAGTAATGAAATCCCTTCCACAGACGTCACTGATAAAACCGGTCGGGAACATCTCTCGGTCTATGCTGTGGTGGTGATTGCGTCTGTGG
 373   A  N  D  I  G  D  T  T  N  R  S  N  E  I  P  S  T  D  V  T  D  K  T  G  R  E  H  L  S  V  Y  A  V  V  V  I  A  S  V  V

1441 TGGGATTTTGCCTTTTGGTAATGCTGTTTCTGCTTAAGTTGGCAAGACACTCCAAGTTTGGCATGAAAGGCCCAGCCTCCGTTATCAGCAATGATGATGACTCTGCCAGCCCACTCCATC
 413   G  F  C  L  L  V  M  L  F  L  L  K  L  A  R  H  S  K  F  G  M  K  G  P  A  S  V  I  S  N  D  D  D  S  A  S  P  L  H  H

1561 ACATCTCCAATGGGAGTAACACTCCATCTTCTTCGGAAGGTGGCCCAGATGCTGTCATTATTGGAATGACCAAGATCCCTGTCATTGAAAATCCCCAGTACTTTGGCATCACCAACAGTC
 453   I  S  N  G  S  N  T  P  S  S  S  E  G  G  P  D  A  V  I  I  G  M  T  K  I  P  V  I  E  N  P  Q  Y  F  G  I  T  N  S  Q
```

FIG. 1A

```
1681 AGCTCAAGCCAGACACATTTGTTCAGCACATCAAGCGACATAACATTGTTCTGAAAAGGGAGCTAGGCGAAGGAGCCTTTGGAAAAGTGTTCCTAGCTGAATGCTATAACCTCTGTCCTG
 493   L  K  P  D  T  F  V  Q  H  I  K  R  H  N  I  V  L  K  R  E  L  G  E  G  A  F  G  K  V  F  L  A  E  C  Y  N  L  C  P  E

1801 AGCAGGACAAGATCTTGGTGGCAGTGAAGACCCTGAAGGATGCCAGTGACAATGCACGCAAGGACTTCCACCGTGAGGCCGAGCTCCTGACCAACCTCCAGCATGAGCACATCGTCAAGT
 533   Q  D  K  I  L  V  A  V  K  T  L  K  D  A  S  D  N  A  R  K  D  F  H  R  E  A  E  L  L  T  N  L  Q  H  E  H  I  V  K  F

1921 TCTATGGCGTCTGCGTGGAGGGCGACCCCCTCATCATGGTCTTTGAGTACATGAAGCATGGGGACCTCAACAAGTTCCTCAGGGCACACGGCCCTGATGCCGTGCTGATGGCTGAGGGCA
 573   Y  G  V  C  V  E  G  D  P  L  I  M  V  F  E  Y  M  K  H  G  D  L  N  K  F  L  R  A  H  G  P  D  A  V  L  M  A  E  G  N

2041 ACCCGCCCACGGAACTGACGCAGTCGCAGATGCTGCATATAGCCCAGCAGATCGCCGCGGGCATGGTCTACCTGGCGTCCCAGCACTTCGTGCACCGCGATTTGGCCACCAGGAACTGCC
 613   P  P  T  E  L  T  Q  S  Q  M  L  H  I  A  Q  Q  I  A  A  G  M  V  Y  L  A  S  Q  H  F  V  H  R  D  L  A  T  R  N  C  L

2161 TGGTCGGGGAGAACTTGCTGGTGAAAATCGGGGACTTTGGGATGTCCCGGGACGTGTACAGCACTGACTACTACAGGGTCGGTGGCCACACAATGCTGCCCATTCGCTGGATGCCTCCAG
 653   V  G  E  N  L  L  V  K  I  G  D  F  G  M  S  R  D  V  Y  S  T  D  Y  Y  R  V  G  G  H  T  M  L  P  I  R  W  M  P  P  E

2281 AGAGCATCATGTACAGGAAATTCACGACGGAAAGCGACGTCTGGAGCCTGGGGGTCGTGTTGTGGGAGATTTTCACCTATGGCAAACAGCCCTGGTACCAGCTGTCAAACAATGAGGTGA
 693   S  I  M  Y  R  K  F  T  T  E  S  D  V  W  S  L  G  V  V  L  W  E  I  F  T  Y  G  K  Q  P  W  Y  Q  L  S  N  N  E  V  I

2401 TAGAGTGTATCACTCAGGGCCGAGTCCTGCAGCGACCCCGCACGTGCCCCCAGGAGGTGTATGAGCTGATGCTGGGGTGCTGGCAGCGAGAGCCCCACATGAGGAAGAACATCAAGGGCA
 733   E  C  I  T  Q  G  R  V  L  Q  R  P  R  T  C  P  Q  E  V  Y  E  L  M  L  G  C  W  Q  R  E  P  H  M  R  K  N  I  K  G  I

2521 TCCATACCCTCCTTCAGAACTTGGCCAAGGCATCTCCGGTCTACCTGGACATTCTAGGCTAGGGCCCTTTTCCCCAGACCGATCCTTCCCAACGTACTCCTCAGACGGGCTGAGAGGATG
 773   H  T  L  L  Q  N  L  A  K  A  S  P  V  Y  L  D  I  L  G  O

2641 AACATCTTTTAACTGCCGCTGGAGGCCACCAAGCTGCTCTCCTTCACTCTGACAGTATTAACATCAAAGACTCCGAGAAGCTCTCGAGGGAAGCAGTGTGTACTTCTTCATCCATAGACA

2761 CAGTATTGACTTCTTTTTGGCATTATCTCTTTCTCTCTTTCCATCTCCCTTGGTTGTTCCTTTTTCTTTTTTTAAATTTTCTTTTTCTTCTTTTTTTTCGTCTTCCCTGCTTCACGATTC

2881 TTACCCTTTCTTTTGAATCAATCTGGCTTCTGCATTACTATTAACTCTGCATAGACAAAGGCCTTAACAAACGTAATTTGTTATATCAGCAGACACTCCAGTTTGCCCACCACAACTAAC

3001 AATGCCTTGTTGTATTCCTGCCTTTGATGTGGATGAAAAAAAGGGAAAACAAATATTTCACTTAAACTTTGTCACTTCTGCTGTACAGATATCGAGAGTTTCTATGGATTCACTTCTATT

3121 TATTTATTATTATTACTGTTCTTATTGTTTTTGGATGGCTTAAGCCTGTGTATAAAAAAAAAAAAAAAATCTAGA
```

FIG. 1B

```
1511 TTTTGTTTTGTTTCATAAGATCCCACTGGATGGGTAGCTGAAATAAAGGAAAAGACAGAGAAAGGGGCTGTGGTGCTTGTTGGTTGATGCTGCCATGTAAGCTGGACTCCTGGGACTGCT
 436  F  V  L  F  H  K  I  P  L  D  G  O

1631 GTTGGCTTATCCCGGGAAGTGCTGCTTATCTGGGGTTTTCTGGTAGATGTGGGCGGTGTTTGGAGGCTGTACTATATGAAGCCTGCATATACTGTGAGCTGTGATTGGGGAACACCAATG

1751 CAGAGGTAACTCTCAGGCAGCTAAGCAGCACCTCAAGAAAACATGTTAAATTAATGCTTCTCTTCTTACAGTAGTTCAAATACAAAACTGAAATGAAATCCCATTGGATTGTACTTCTCT
```

FIG. 1C

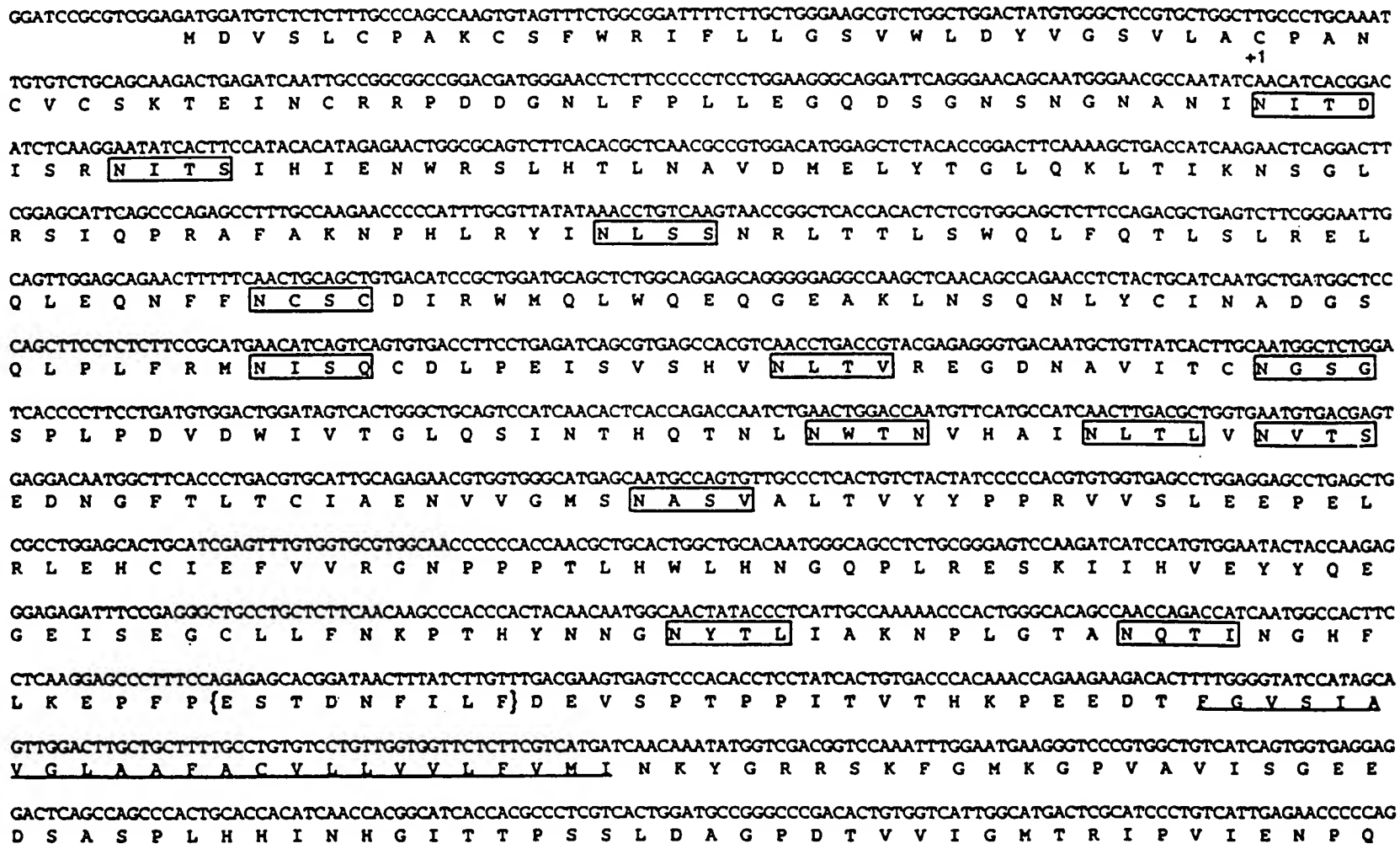

1 GGATCCGCGTCGGAGATGGATGTCTCTCTTTGCCCAGCCAAGTGTAGTTTCTGGCGGATTTTCTTGCTGGGAAGCGTCTGGCTGGACTATGTGGGCTCCGTGCTGGCTTGCCCTGCAAAT
-31 M D V S L C P A K C S F W R I F L L G S V W L D Y V G S V L A C P A N
+1
121 TGTGTCTGCAGCAAGACTGAGATCAATTGCCGGCGGCCGGACGATGGGAACCTCTTCCCCCTCCTGGAAGGGCAGGATTCAGGGAACAGCAATGGGAACGCCAATATCAACATCACGGAC
5 C V C S K T E I N C R R P D D G N L F P L L E G Q D S G N S N G N A N I N I T D
241 ATCTCAAGGAATATCACTTCCATACACATAGAGAACTGGCGCAGTCTTCACACGCTCAACGCCGTGGACATGGAGCTCTACACCGGACTTCAAAAGCTGACCATCAAGAACTCAGGACTT
45 I S R N I T S I H I E N W R S L H T L N A V D M E L Y T G L Q K L T I K N S G L
361 CGGAGCATTCAGCCCAGAGCCTTTGCCAAGAACCCCCATTTGCGTTATATAAACCTGTCAAGTAACCGGCTCACCACACTCTCGTGGCAGCTCTTCCAGACGCTGAGTCTTCGGGAATTG
85 R S I Q P R A F A K N P H L R Y I N L S S N R L T T L S W Q L F Q T L S L R E L
481 CAGTTGGAGCAGAACTTTTTCAACTGCAGCTGTGACATCCGCTGGATGCAGCTCTGGCAGGAGCAGGGGGAGGCCAAGCTCAACAGCCAGAACCTCTACTGCATCAATGCTGATGGCTCC
125 Q L E Q N F F N C S C D I R W M Q L W Q E Q G E A K L N S Q N L Y C I N A D G S
601 CAGCTTCCTCTCTTCCGCATGAACATCAGTCAGTGTGACCTTCCTGAGATCAGCGTGAGCCACGTCAACCTGACCGTACGAGAGGGTGACAATGCTGTTATCACTTGCAATGGCTCTGGA
165 Q L P L F R M N I S Q C D L P E I S V S H V N L T V R E G D N A V I T C N G S G
721 TCACCCCTTCCTGATGTGGACTGGATAGTCACTGGGCTGCAGTCCATCAACACTCACCAGACCAATCTGAACTGGACCAATGTTCATGCCATCAACTTGACGCTGGTGAATGTGACGAGT
205 S P L P D V D W I V T G L Q S I N T H Q T N L N W T N V H A I N L T L V N V T S
841 GAGGACAATGGCTTCACCCTGACGTGCATTGCAGAGAACGTGGTGGGCATGAGCAATGCCAGTGTTGCCCTCACTGTCTACTATCCCCCACGTGTGGTGAGCCTGGAGGAGCCTGAGCTG
245 E D N G F T L T C I A E N V V G M S N A S V A L T V Y Y P P R V V S L E E P E L
961 CGCCTGGAGCACTGCATCGAGTTTGTGGTGCGTGGCAACCCCCCACCAACGCTGCACTGGCTGCACAATGGGCAGCCTCTGCGGGAGTCCAAGATCATCCATGTGGAATACTACCAAGAG
285 R L E H C I E F V V R G N P P P T L H W L H N G Q P L R E S K I I H V E Y Y Q E
1081 GGAGAGATTTCCGAGGGCTGCCTGCTCTTCAACAAGCCCACCCACTACAACAATGGCAACTATACCCTCATTGCCAAAAACCCACTGGGCACAGCCAACCAGACCATCAATGGCCACTTC
325 G E I S E G C L L F N K P T H Y N N G N Y T L I A K N P L G T A N Q T I N G H F
1201 CTCAAGGAGCCCTTTCCAGAGAGCACGGATAACTTTATCTTGTTTGACGAAGTGAGTCCCACACCTCCTATCACTGTGACCCACAAACCAGAAGAAGACACTTTTGGGGTATCCATAGCA
365 L K E P F P {E S T D N F I L F} D E V S P T P P I T V T H K P E E D T F G V S I A
1321 GTTGGACTTGCTGCTTTTGCCTGTGTCCTGTTGGTGGTTCTCTTCGTCATGATCAACAAATATGGTCGACGGTCCAAATTTGGAATGAAGGGTCCCGTGGCTGTCATCAGTGGTGAGGAG
405 V G L A A F A C V L L V V L F V M I N K Y G R R S K F G M K G P V A V I S G E E
1441 GACTCAGCCAGCCCACTGCACCACATCAACCACGGCATCACCACGCCCTCGTCACTGGATGCCGGGCCCGACACTGTGGTCATTGGCATGACTCGCATCCCTGTCATTGAGAACCCCCAG
445 D S A S P L H H I N H G I T T P S S L D A G P D T V V I G M T R I P V I E N P Q

FIG. 2A

FIG. 2B

```
1600 TGGGTCTTTTCAAACATAGACAATCATGGGATATTAAACTTGAAGGACAATAGAGATCATCTAGTCCCATCAACTCACTATATATATGAGGAACCTGAGGTCCAGAGTGGGGAAGTGTCT
 498 W  V  F  S  N  I  D  N  H  G  I  L  N  L  K  D  N  R  D  H  L  V  P  S  T  H  Y  I  Y  E  E  P  E  V  Q  S  G  E  V  S

1720 TACCCAAGGTCACATGGTTTCAGAGAAATTATGTTGAATCCAATAAGCCTTCCCGGACATTCCAAGCCTCTTAACCATGGCATCTATGTTGAGGATGTCAATGTTTATTTCAGCAAAGGA
 538 Y  P  R  S  H  G  F  R  E  I  M  L  N  P  I  S  L  P  G  H  S  K  P  L  N  H  G  I  Y  V  E  D  V  N  V  Y  F  S  K  G

1840 CGTCATGGCTTTTAAAAAC
 578 R  H  G  F  O
```

FIG. 2C

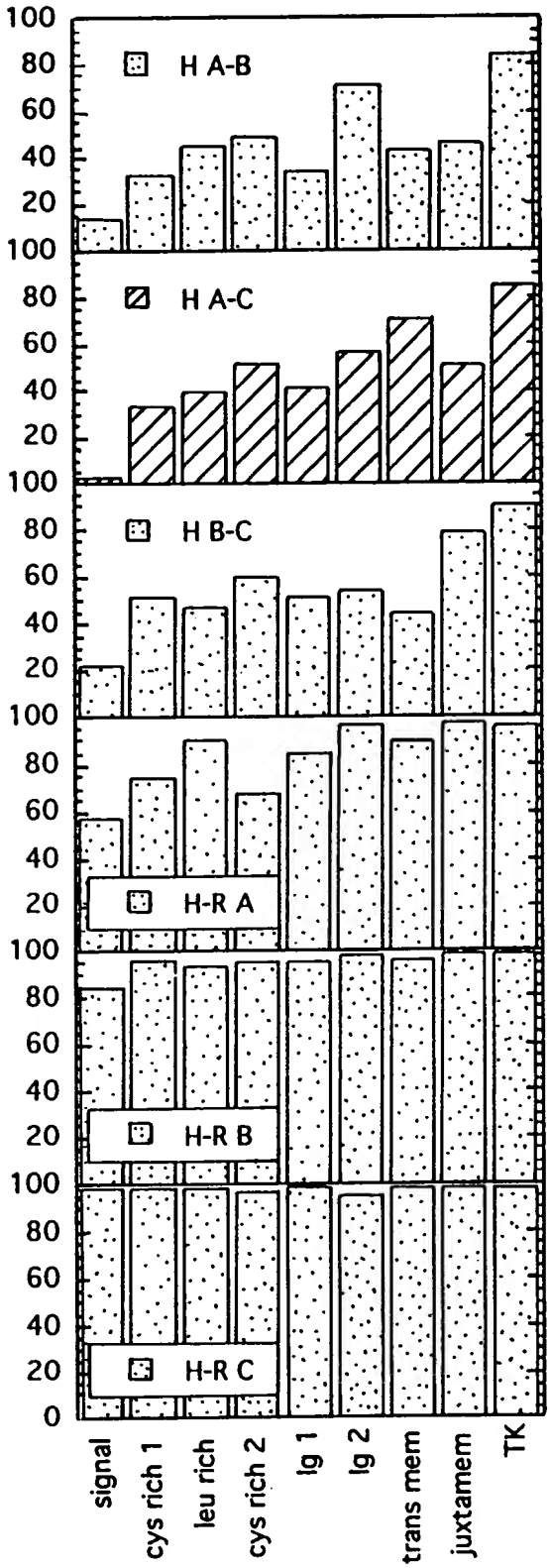


FIG. 3

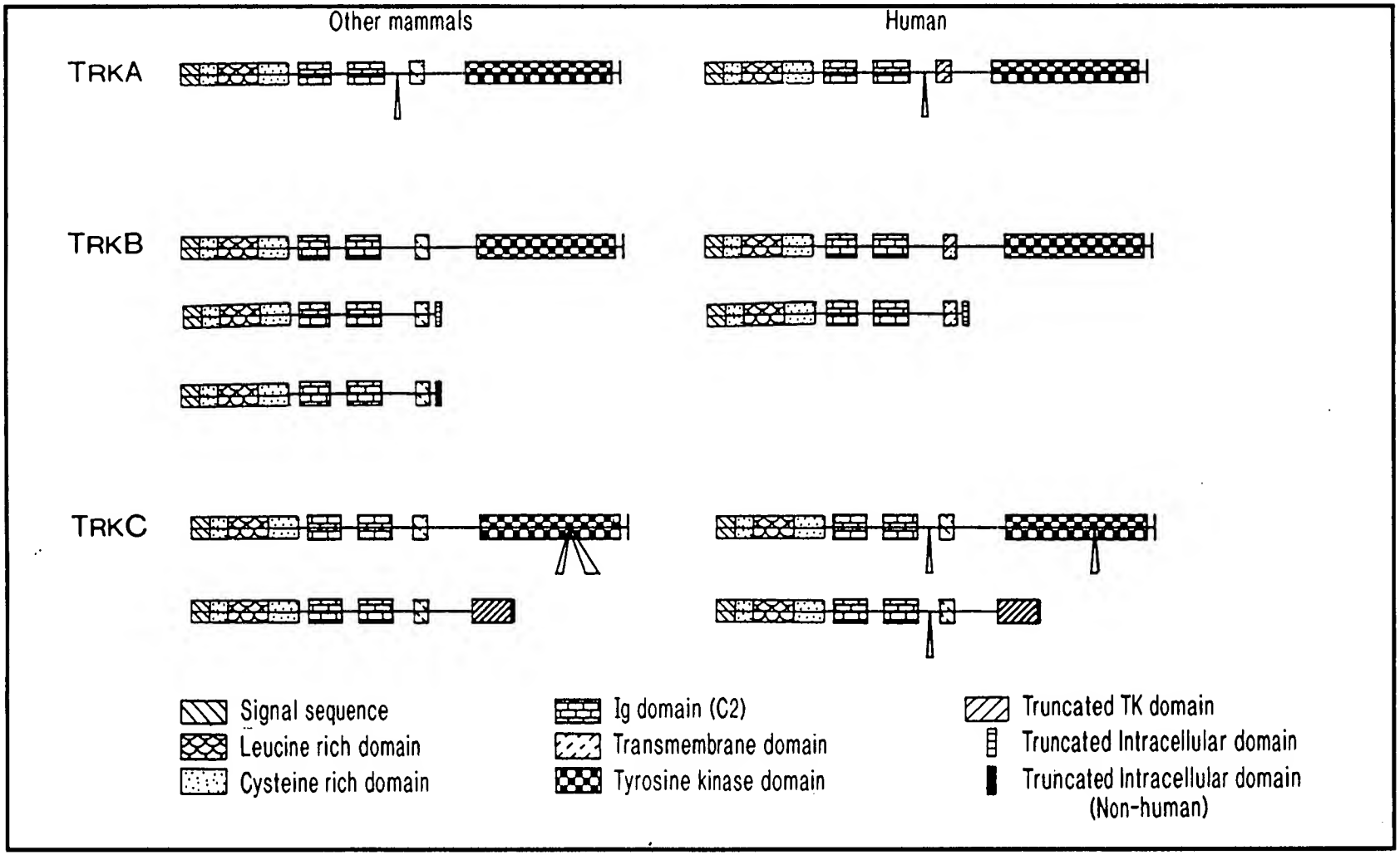


FIG. 4

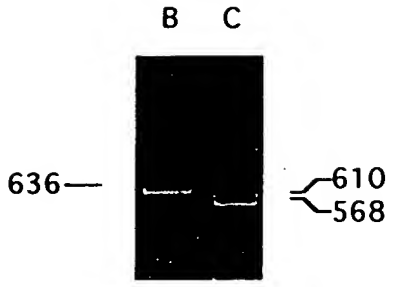

B
C
636
610
568

FIG. 5

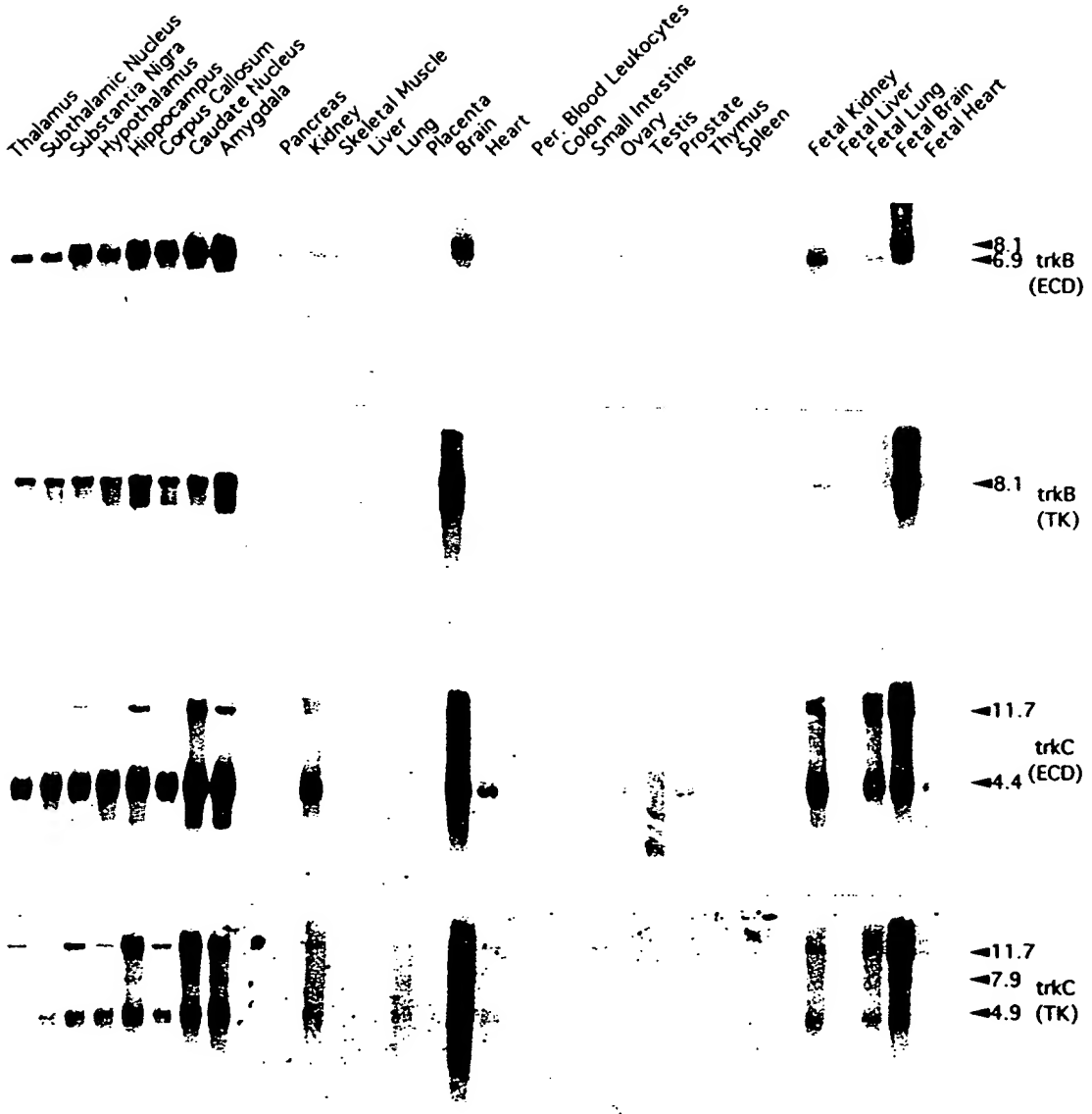

Thalamus
Subthalamic Nucleus
Substantia Nigra
Hypothalamus
Hippocampus
Corpus Callosum
Caudate Nucleus
Amygdala
Pancreas
Kidney
Skeletal Muscle
Liver
Lung
Placenta
Brain
Heart
Per. Blood Leukocytes
Colon
Small Intestine
Ovary
Testis
Prostate
Thymus
Spleen
Fetal Kidney
Fetal Liver
Fetal Lung
Fetal Brain
Fetal Heart
8.1
6.9
trkB (ECD)
8.1
trkB (TK)
11.7
4.4
trkC (ECD)
11.7
7.9
4.9
trkC (TK)

FIG. 6

FIG. 7A

FIG. 7B

FIG. 7C

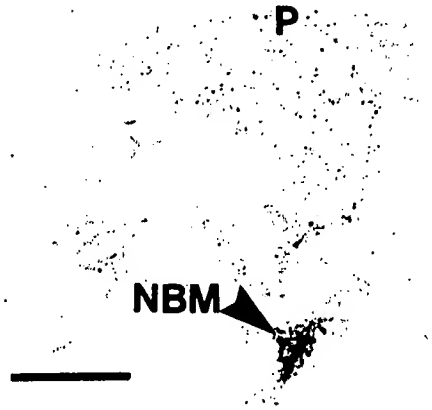


FIG. 7D

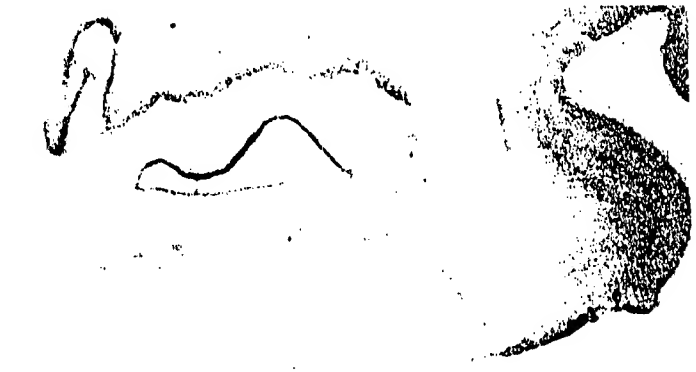


FIG. 7E

FIG. 8A

FIG. 8B

FIG. 8C

FIG. 8D

FIG. 8E

FIG. 8F

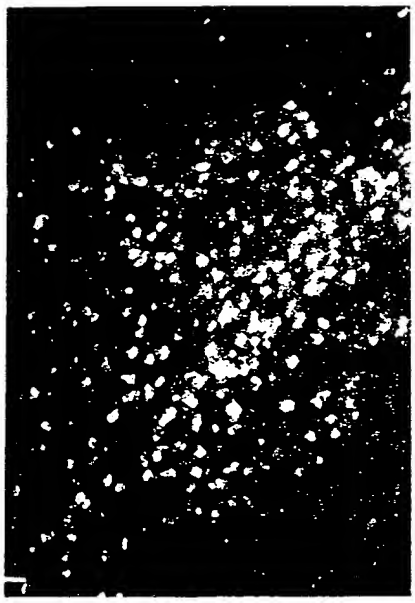


FIG. 9A

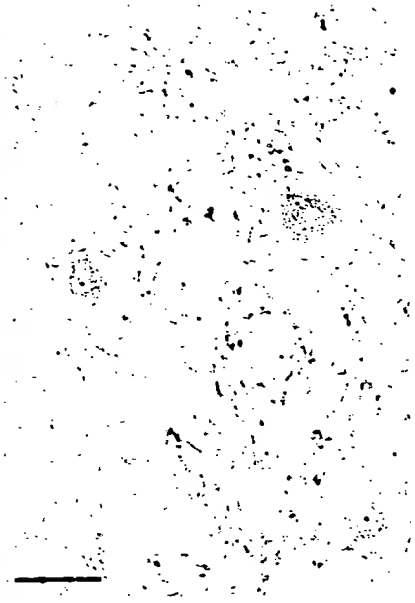


FIG. 9B

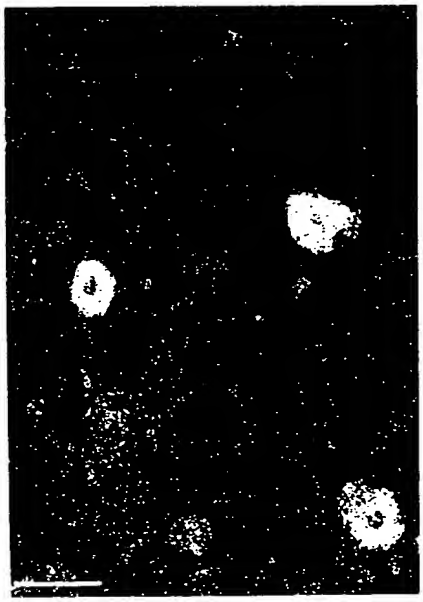


FIG. 9C

FIG. 9D

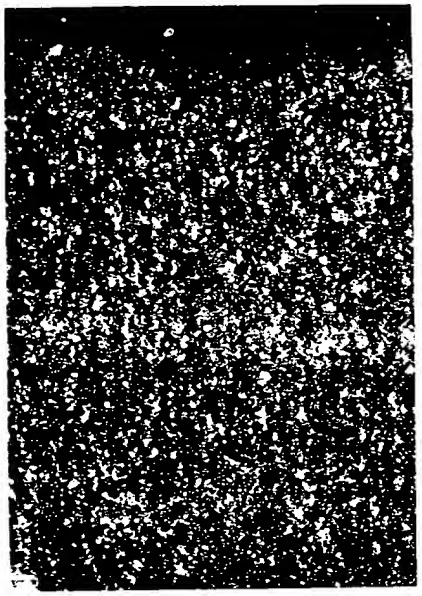


FIG. 9E

FIG. 9F

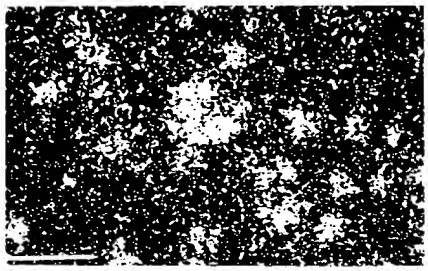


FIG. 9G

FIG. 10A

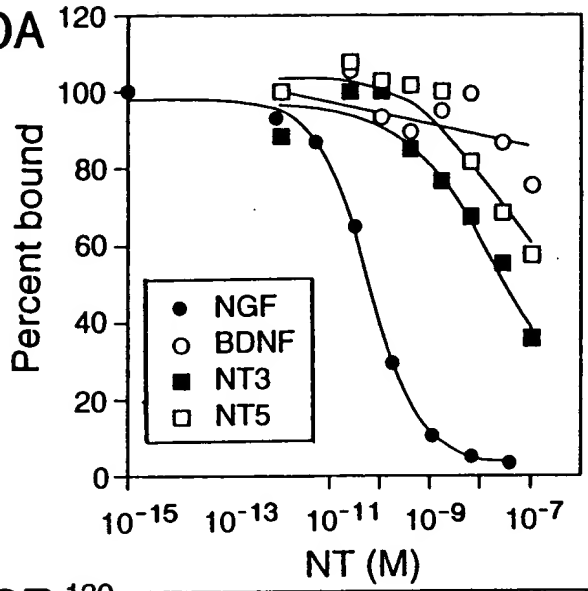


FIG. 10B

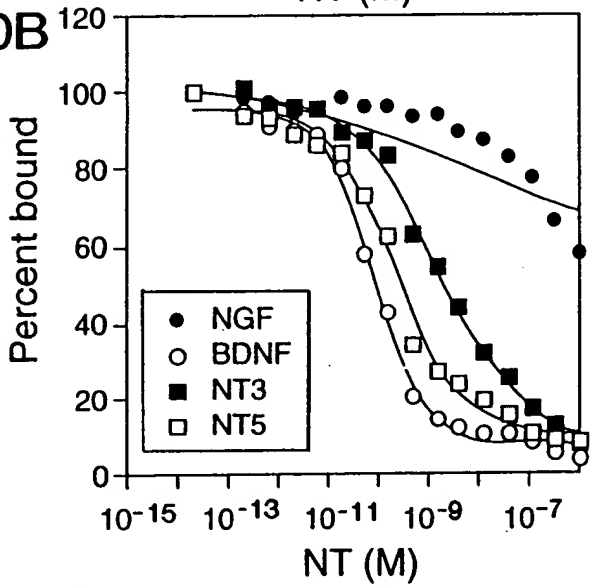


FIG. 10C

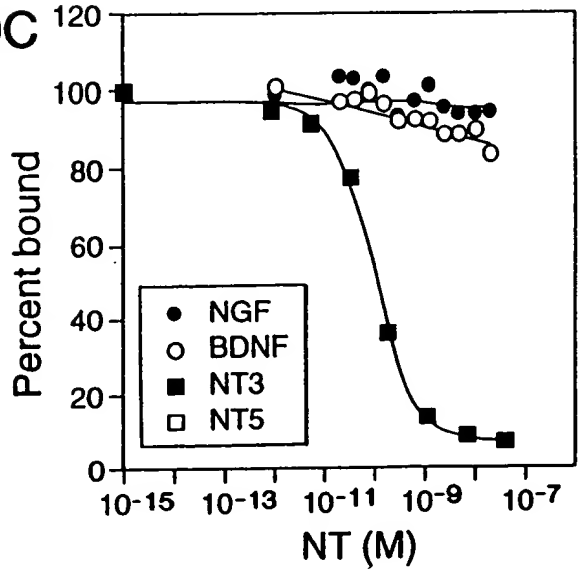


FIG. 11A

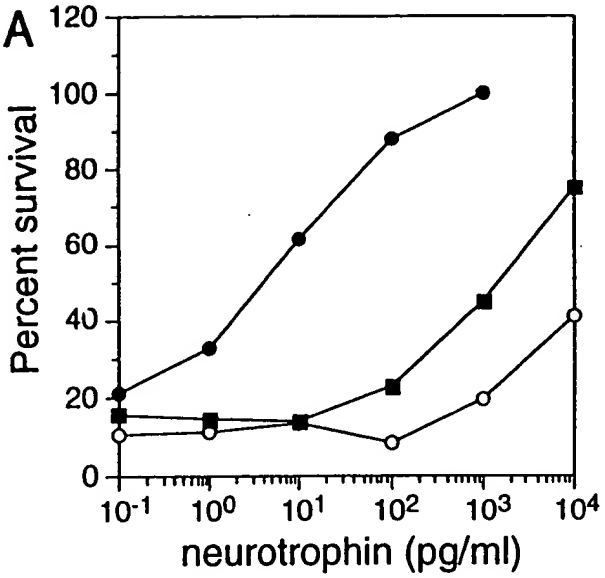


FIG. 11B

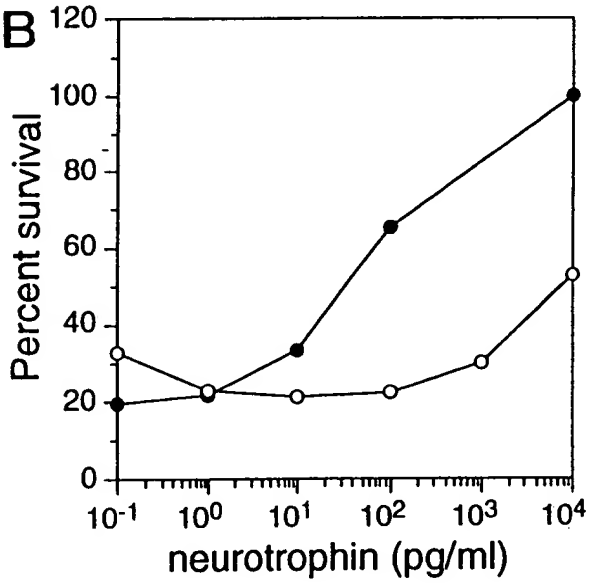
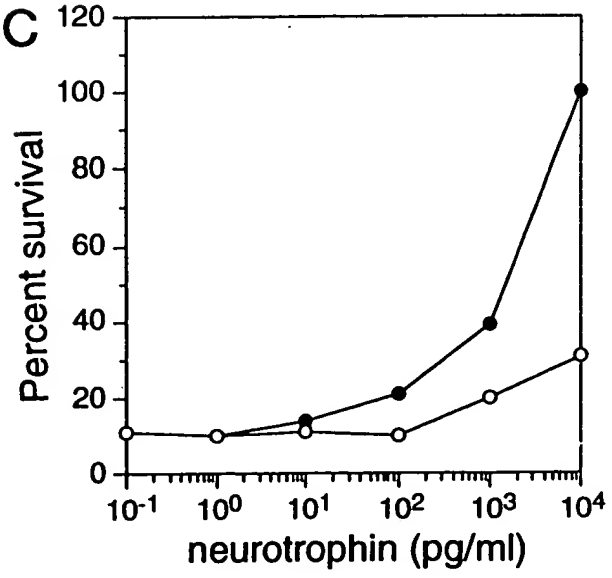


FIG. 11C



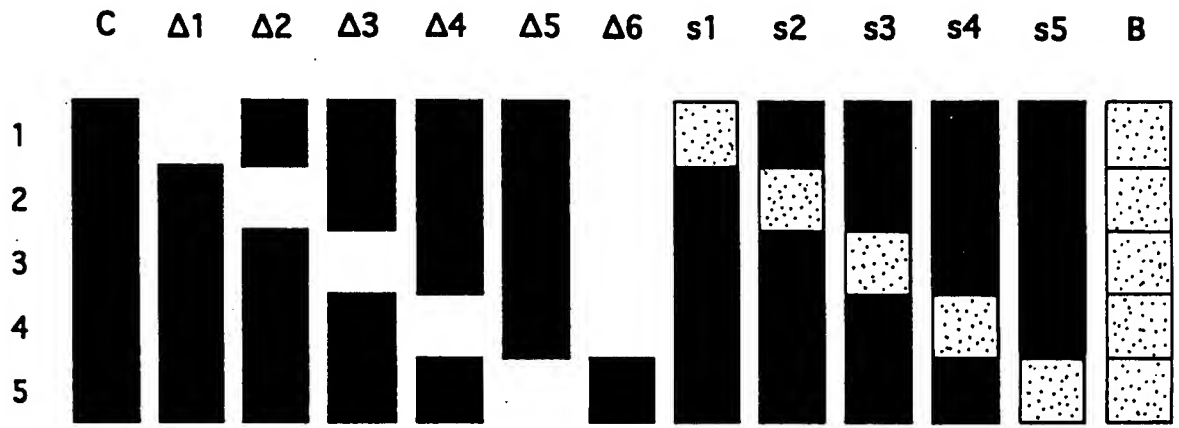


FIG. 12

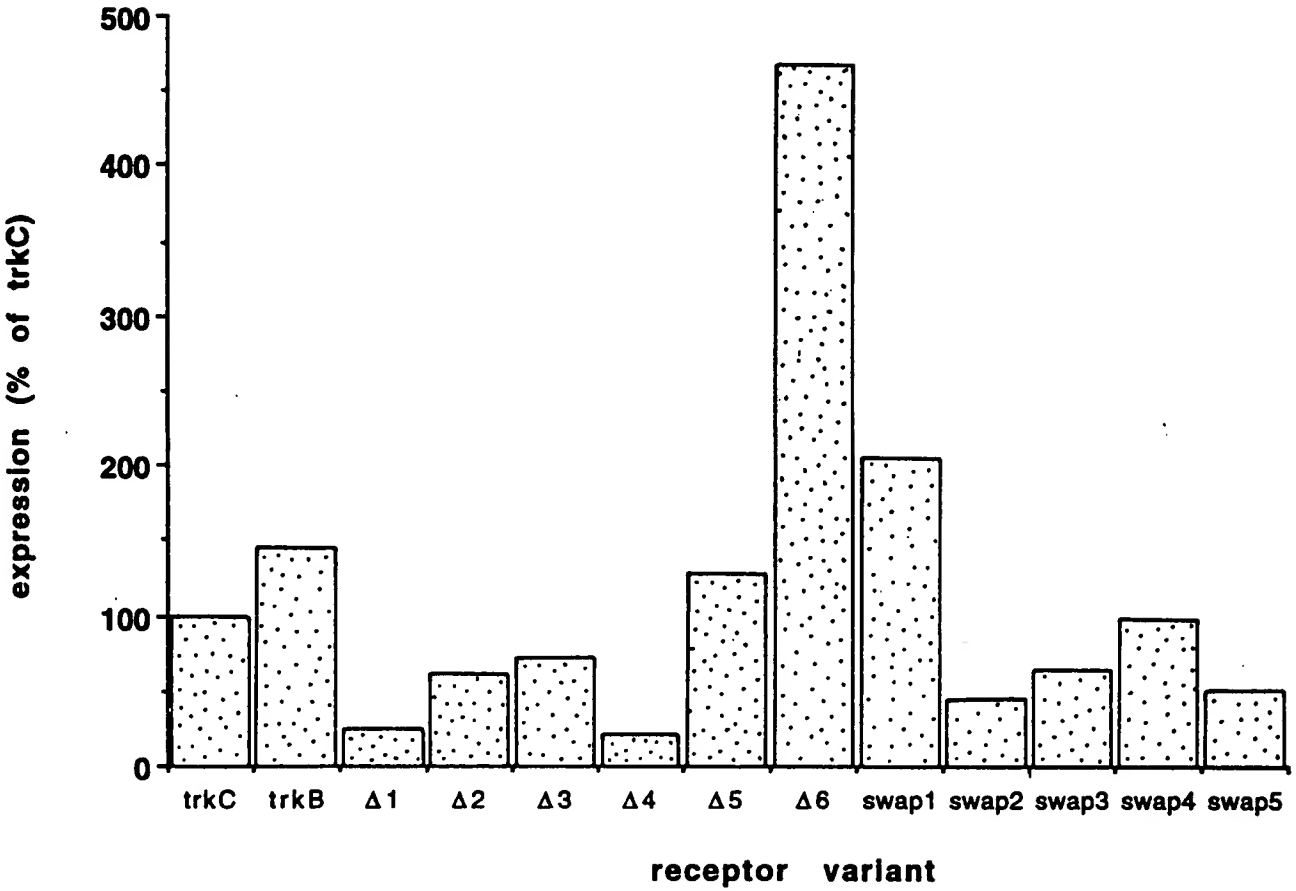


FIG. 13

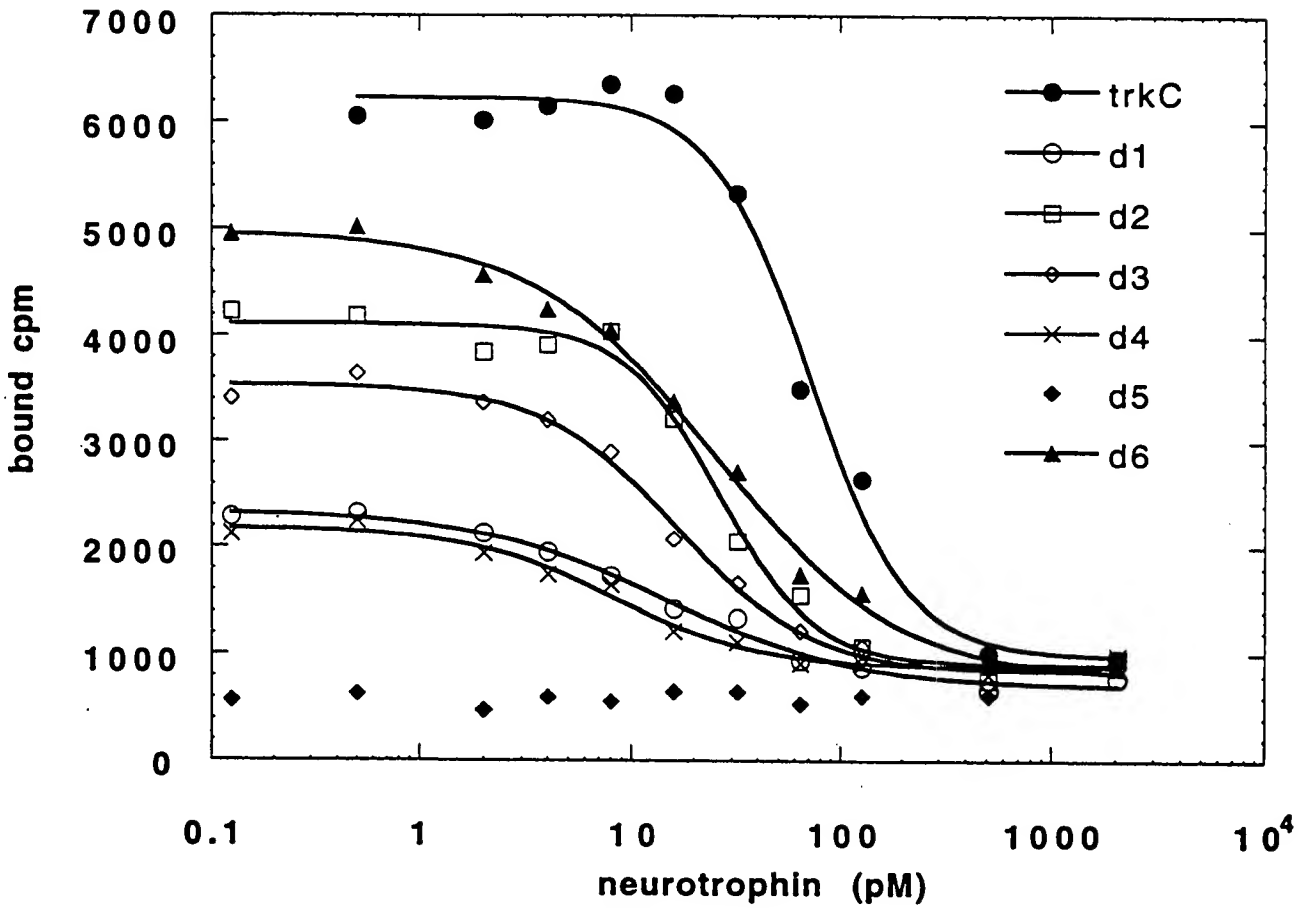

7000
6000
5000
4000
3000
2000
1000
0
bound cpm
0.1
1
10
100
1000
10^4
neurotrophin (pM)
trkC
d1
d2
d3
d4
d5
d6

FIG. 14A

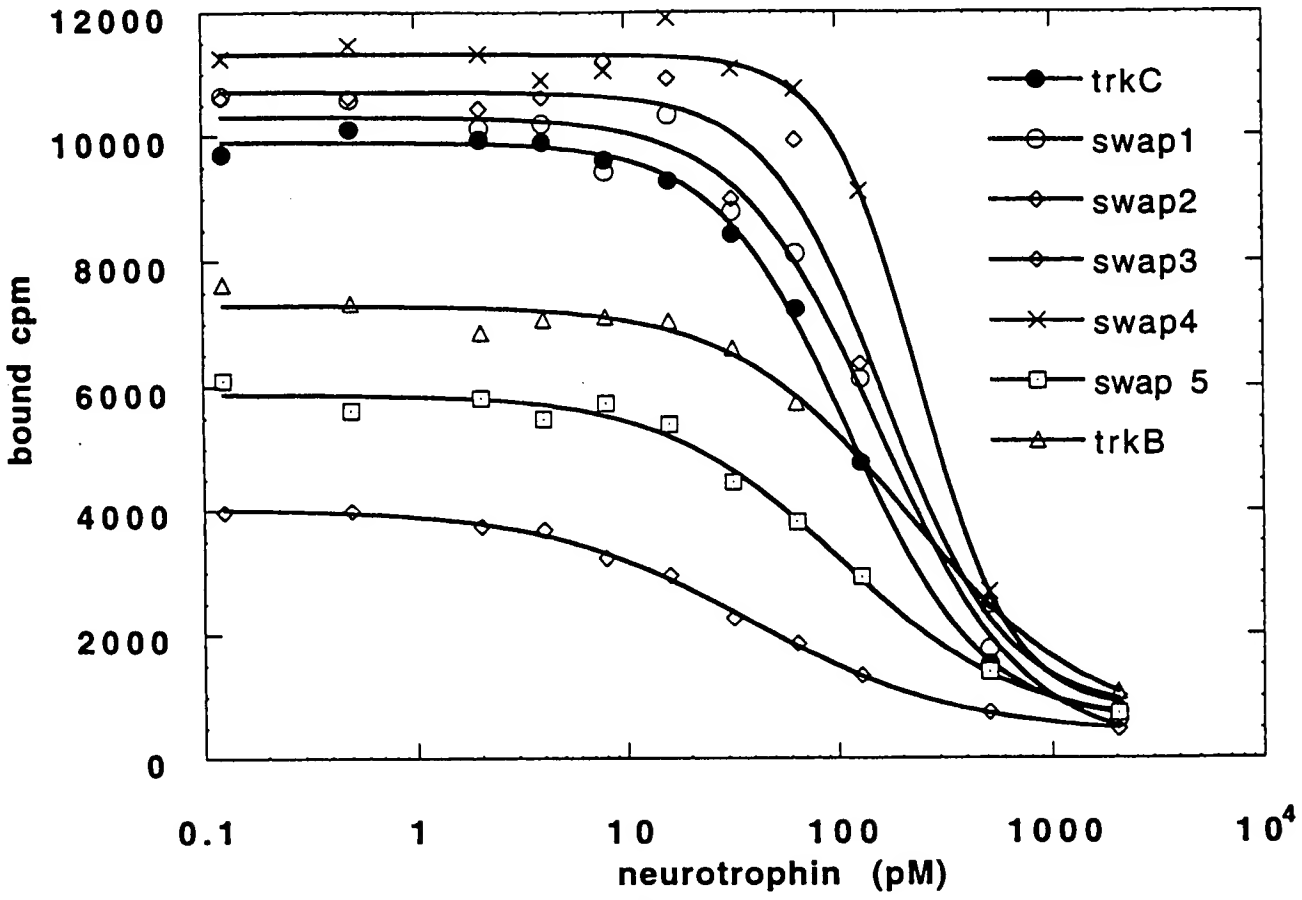


FIG. 14B

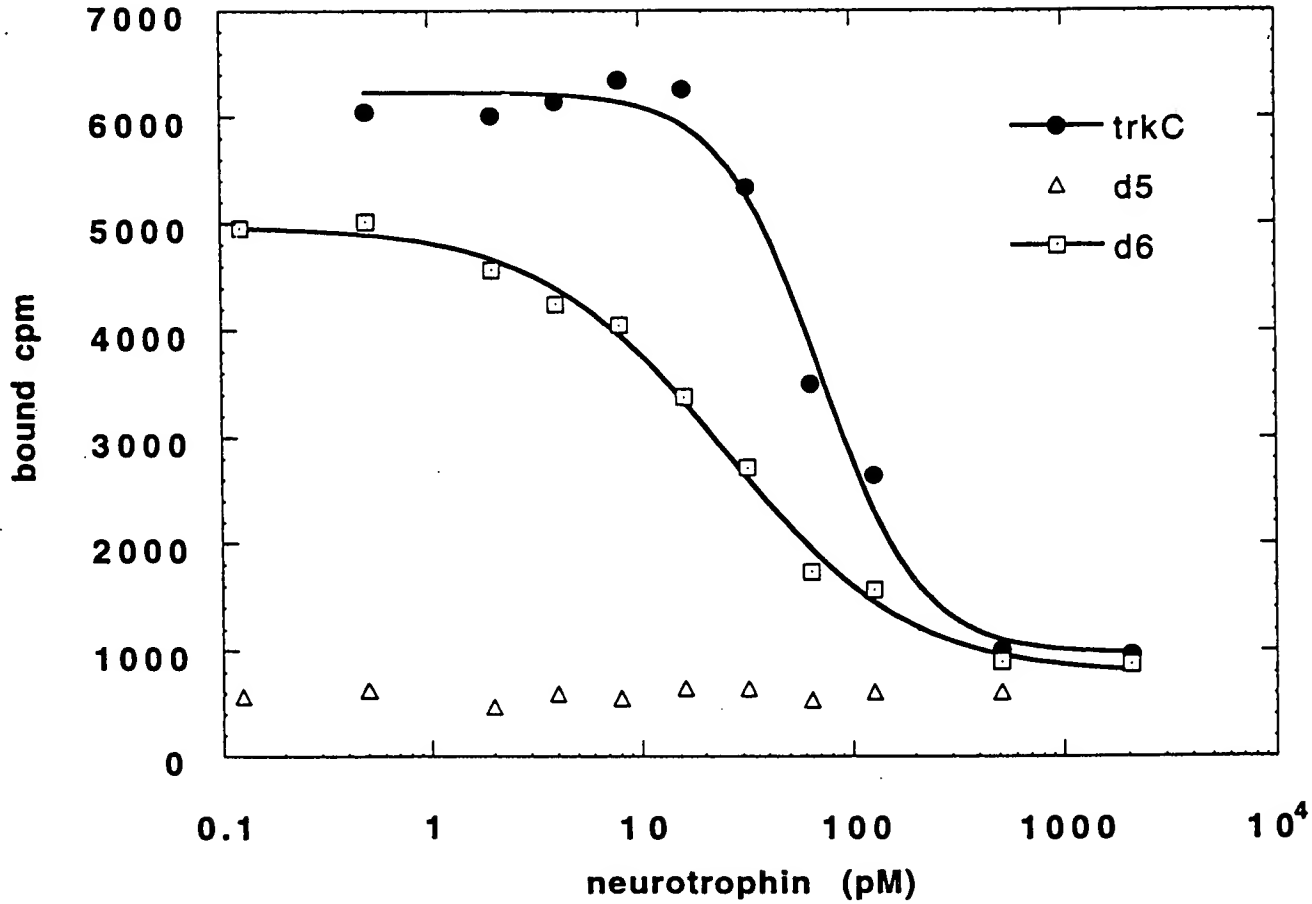


FIG. 14C

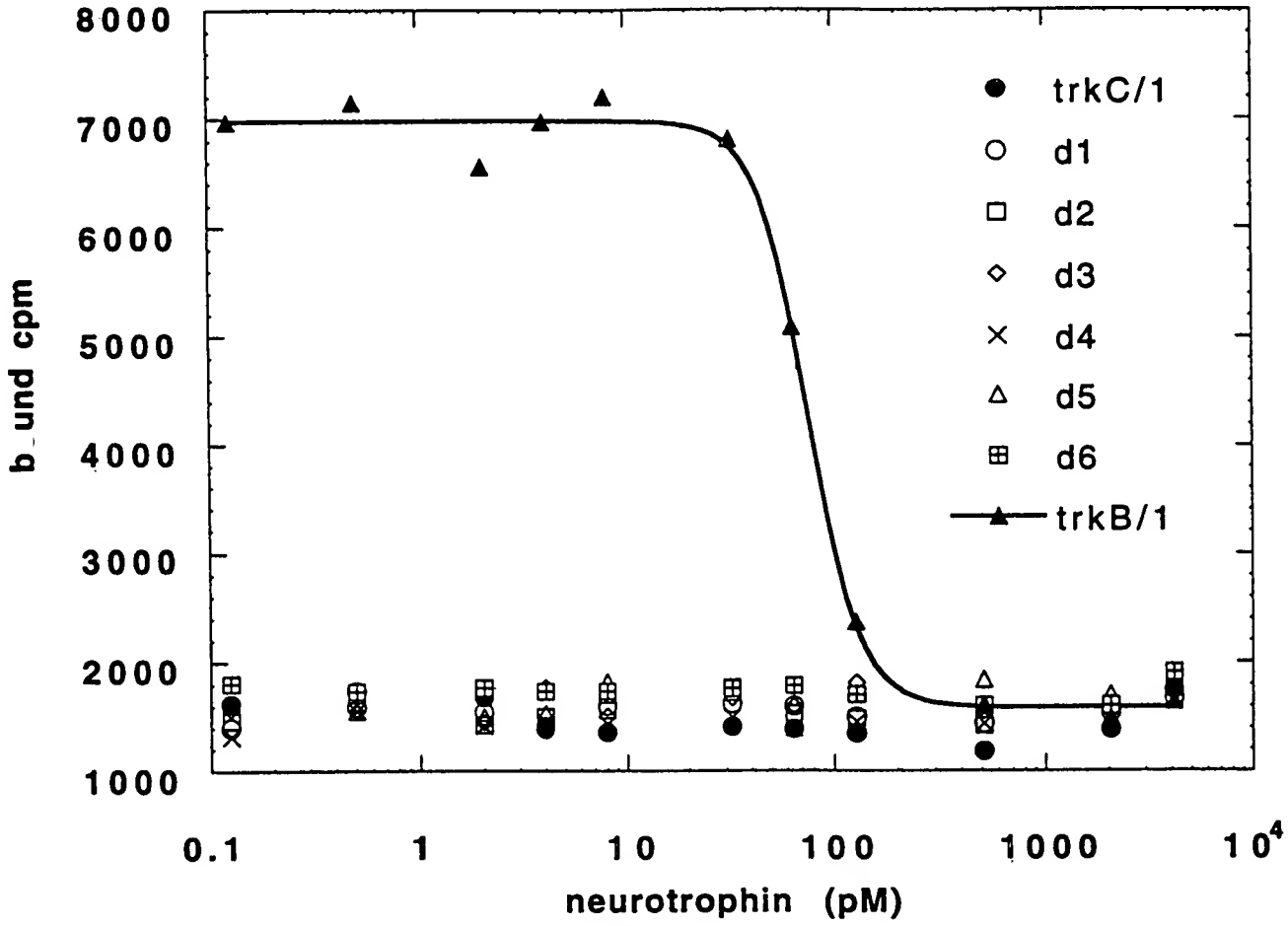


FIG. 15A

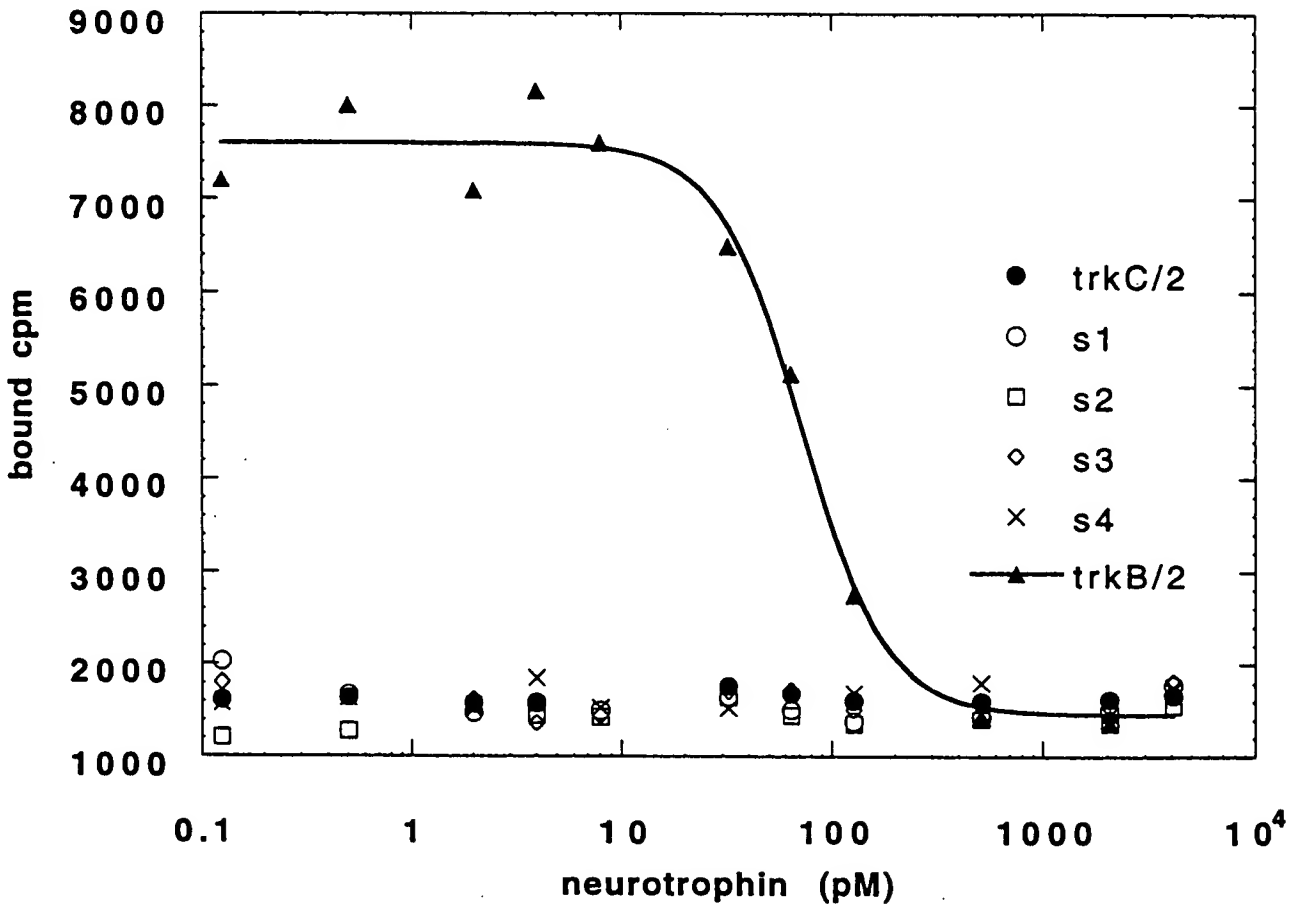


FIG. 15B

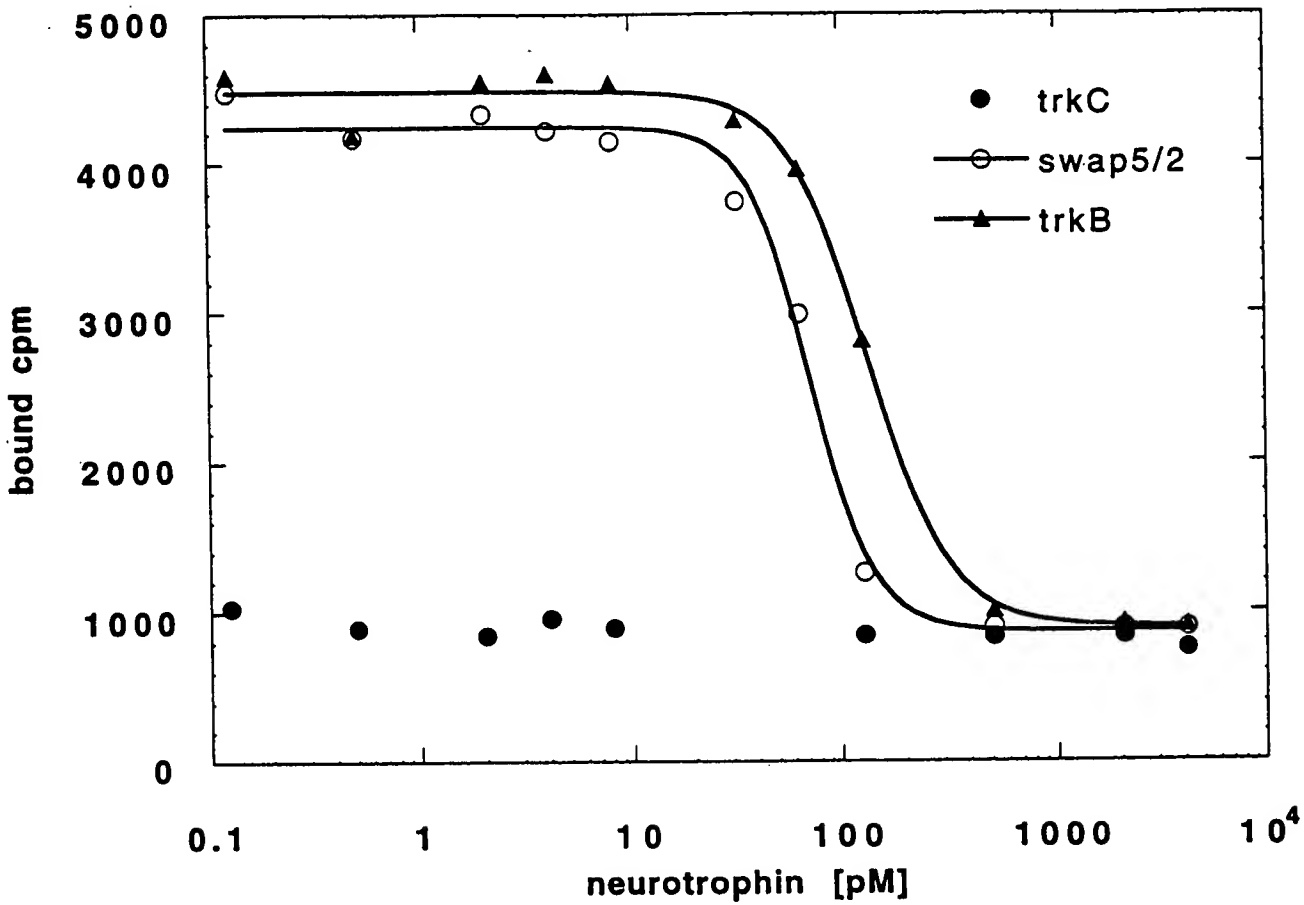


FIG. 15C

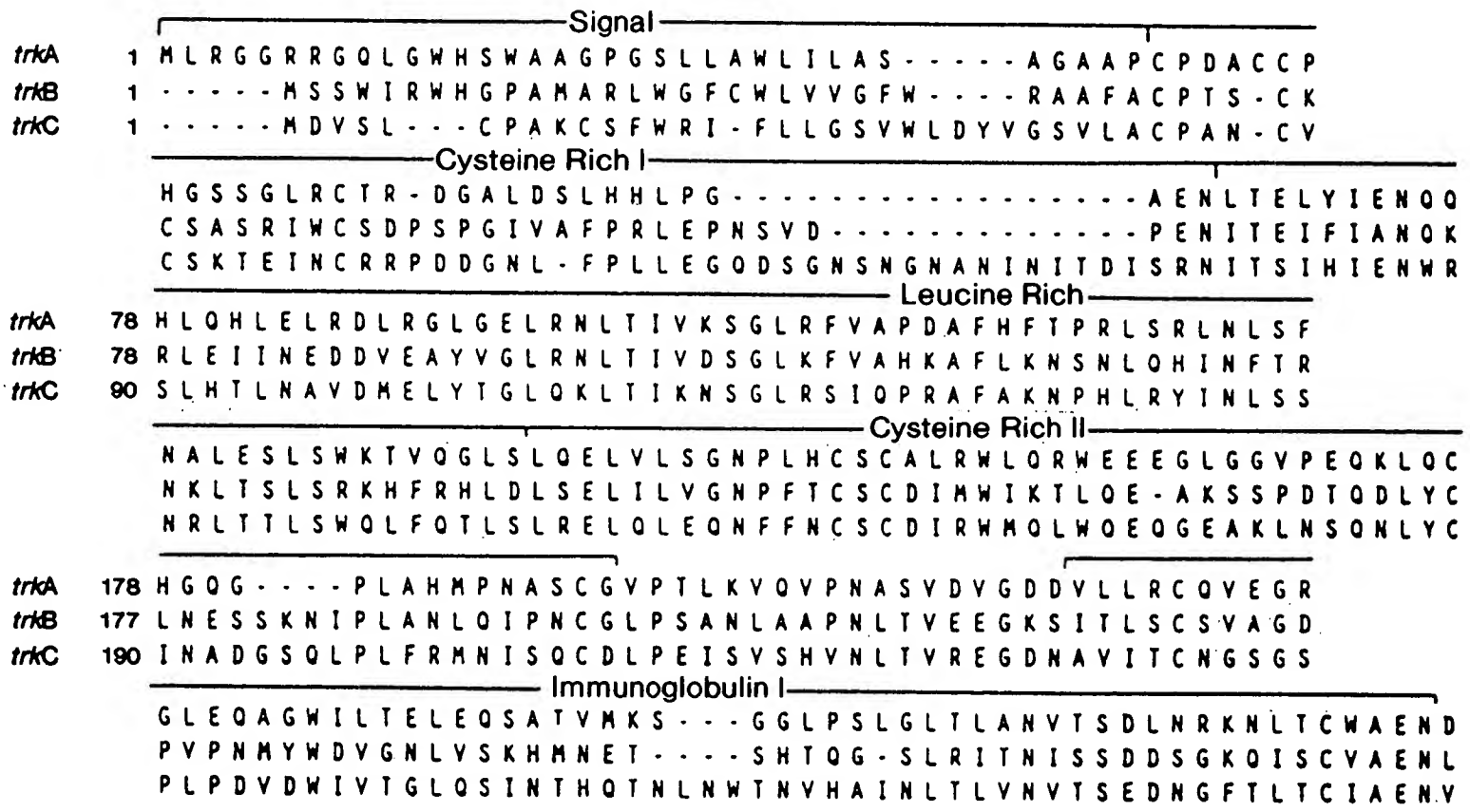

Signal
trkA 1 MLRGGRRGQLGWHSWAAGPGSLLAWLILAS-----AGAAPCPDACCP
trkB 1 -----MSSWIRWHGPAMARLWGFCWLVVGFW----RAAFACPTS-CK
trkC 1 -----MDVSL---CPAKCSFWRI-FLLGSVWLDYVGSVLACPAN-CV
Cysteine Rich I
HGSSGLRCTR-DGALDSLHHLPG----------AENLTELYIENQQ
CSASRIWCSDPSPGIVAFPRLEPNSVD----------PENITEIFIANQK
CSKTEINCRRPDDGNL-FPLLEGQDSGNSNGNANINITDISRNITSIHIENWR
Leucine Rich
trkA 78 HLQHLELRDLRGLGELRNLTIVKSGLRFVAPDAFHFTPRLSRLNLSF
trkB 78 RLEIINEDDVEAYVGLRNLTIVDSGLKFVAHKAFLKNSNLQHINFTR
trkC 90 SLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSS
Cysteine Rich II
NALESLSWKTVQGLSLQELVLSGNPLHCSCALRWLQRWEEEGLGGVPEQKLQC
NKLTSLSRKHFRHLDLSELILVGNPFTCSCDIMWIKTLQE-AKSSPDTQDLYC
NRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYC
trkA 178 HGQG----PLAHMPNASCGVPTLKVQVPNASVDVGDDVLLRCQVEGR
trkB 177 LNESSKNIPLANLQIPNCGLPSANLAAPNLTVEEGKSITLSCSVAGD
trkC 190 INADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGS
Immunoglobulin I
GLEQAGWILTELEQSATVMKS---GGLPSLGLTLANVTSDLNRKNLTCWAEND
PVPNMYWDVGNLVSKHMNET----SHTQG-SLRITNISSDDSGKQISCVAENL
PLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENV

FIG. 16A

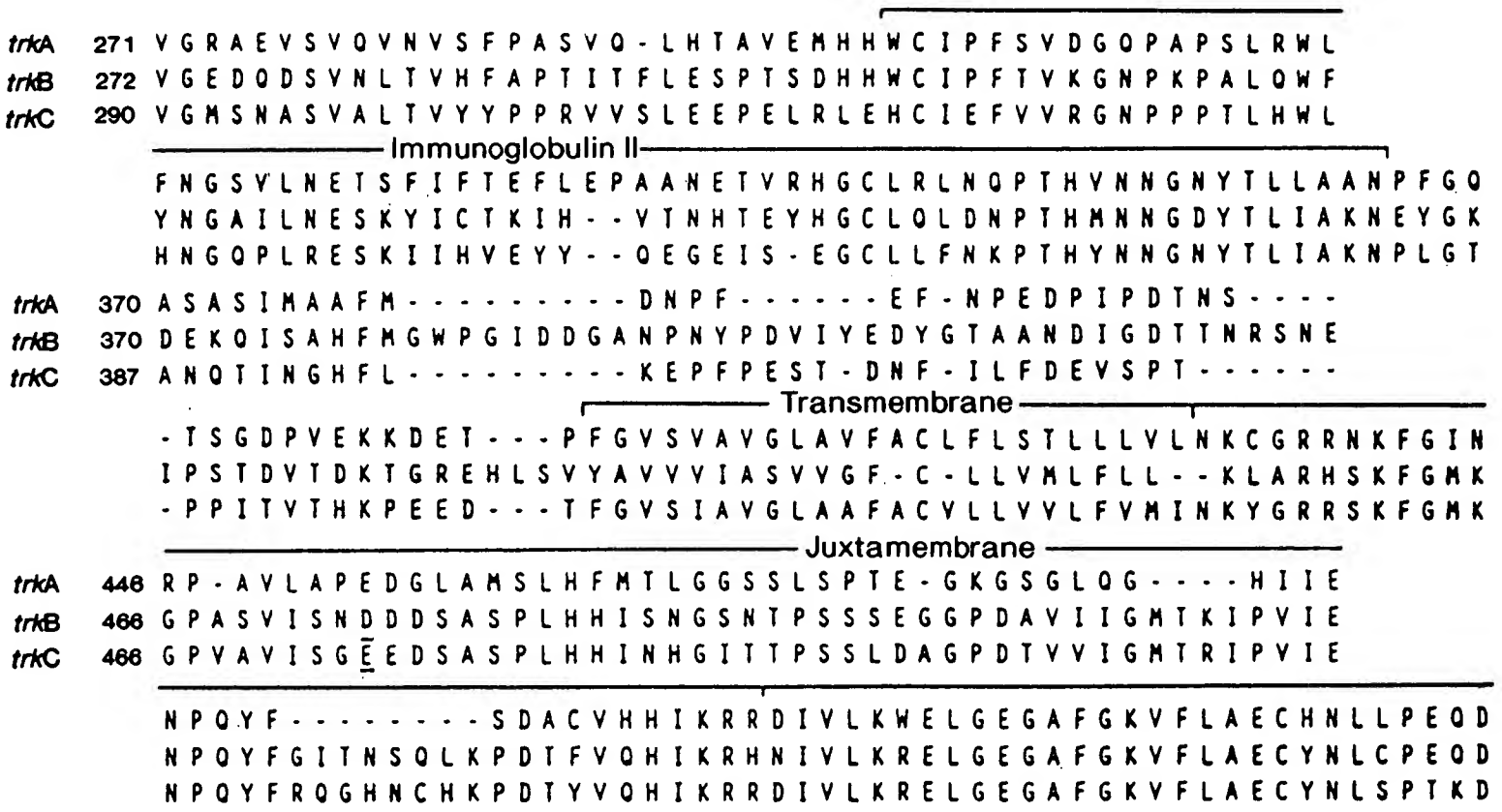

trkA 271 V G R A E V S V Q V N V S F P A S V Q - L H T A V E M H H W C I P F S V D G Q P A P S L R W L
trkB 272 V G E D Q D S V N L T V H F A P T I T F L E S P T S D H H W C I P F T V K G N P K P A L Q W F
trkC 290 V G M S N A S V A L T V Y Y P P R V V S L E E P E L R L E H C I E F V V R G N P P P T L H W L
Immunoglobulin II
F N G S V L N E T S F I F T E F L E P A A N E T V R H G C L R L N Q P T H V N N G N Y T L L A A N P F G Q
Y N G A I L N E S K Y I C T K I H - - V T N H T E Y H G C L Q L D N P T H M N N G D Y T L I A K N E Y G K
H N G Q P L R E S K I I H V E Y Y - - Q E G E I S - E G C L L F N K P T H Y N N G N Y T L I A K N P L G T
trkA 370 A S A S I M A A F M - - - - - - - - - - D N P F - - - - - - E F - N P E D P I P D T N S - - - -
trkB 370 D E K Q I S A H F M G W P G I D D G A N P N Y P D V I Y E D Y G T A A N D I G D T T N R S N E
trkC 387 A N Q T I N G H F L - - - - - - - - - - K E P F P E S T - D N F - I L F D E V S P T - - - - - -
Transmembrane
- T S G D P V E K K D E T - - - P F G V S V A V G L A V F A C L F L S T L L L V L N K C G R R N K F G I N
I P S T D V T D K T G R E H L S V Y A V V V I A S V V G F - C - L L V M L F L L - - K L A R H S K F G M K
- P P I T V T H K P E E D - - - T F G V S I A V G L A A F A C V L L V V L F V M I N K Y G R R S K F G M K
Juxtamembrane
trkA 446 R P - A V L A P E D G L A M S L H F M T L G G S S L S P T E - G K G S G L Q G - - - - H I I E
trkB 466 G P A S V I S N D D D S A S P L H H I S N G S N T P S S S E G G P D A V I I G M T K I P V I E
trkC 466 G P V A V I S G E E D S A S P L H H I N H G I T T P S S L D A G P D T V V I G M T R I P V I E
N P Q Y F - - - - - - - - S D A C V H H I K R R D I V L K W E L G E G A F G K V F L A E C H N L L P E Q D
N P Q Y F G I T N S Q L K P D T F V Q H I K R H N I V L K R E L G E G A F G K V F L A E C Y N L C P E Q D
N P Q Y F R Q G H N C H K P D T Y V Q H I K R R D I V L K R E L G E G A F G K V F L A E C Y N L S P T K D

FIG. 16B

```
trkA  532 KMLVAVKALKEASESARQDFQREAELLTMLQHQHIVRFFGVCTEGRP
trkB  566 KILVAVKTLKDASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDP
trkC  566 KMLVAVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDP
          Tyrosine Kinase
          LLMVFEYMRHGDLNRFLRSHGPDAKLLAGGEDV-APGPLGLGQLLAVASQVAA
          LIMVFEYMKHGDLNKFLRAHGPDAVLMAEGNPP---TELTQSQMLHIAQQIAA
          LIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIAS

trkA  631 GMVYLAGLHFVHRDLATRNCLVGQGLVVKIGDFGMSRDIYSTDYYR-
trkB  663 GMVYLASQHFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYYR-
trkC  666 GMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRL

          ----------------VGGRTMLPIRWMPPESILYRKFTTESDVWSFGVVLWEIFT
          ----------------VGGHTMLPIRWMPPESIMYRKFTTESDVWSLGVVLWEIFT
          FNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFT

trkA  717 YGKQPWYQLSNTEAIDCITQGRELERPRACPPEVYAIMRGCWQREPQ
trkB  749 YGKQPWYQLSNNEVIECITQGRVLQRPRTCPQEVYELMLGCWQREPH
trkC  766 YGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQ

          QRHSIKDVHARLQALAQAPPVYLDVLG
          MRKNIKGIHTLLQNLAKASPVYLDILG
          QRLNIKEIYKILHALGKATPIYLDILG
```

FIG. 16C

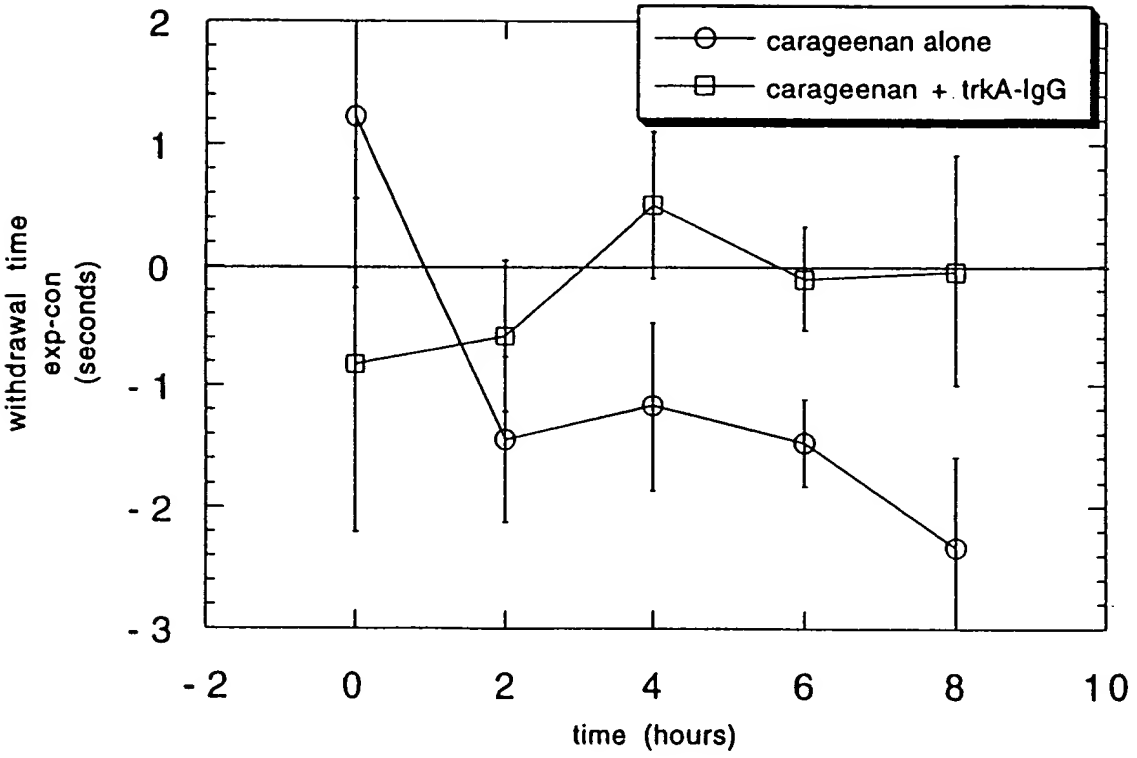


FIG. 17

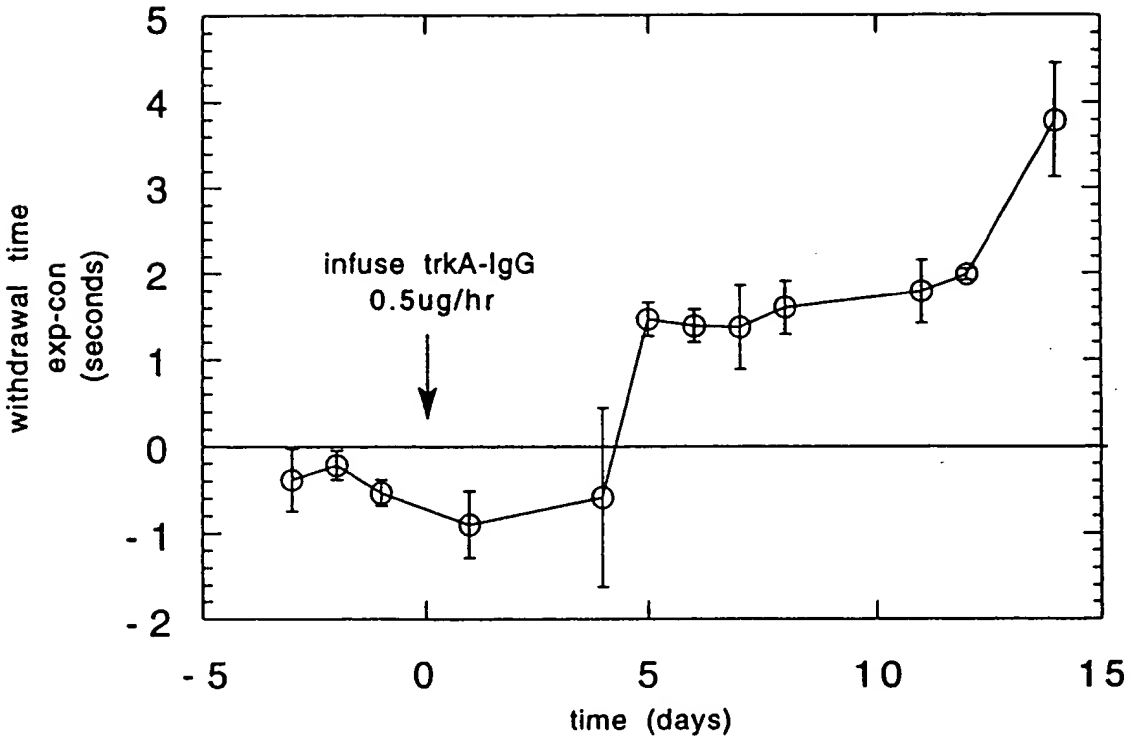

withdrawal time
exp-con
(seconds)
infuse trkA-IgG
0.5ug/hr
time (days)
5
4
3
2
1
0
-1
-2
-5
0
5
10
15

FIG. 18